



SEQUENCE LISTING

<110> Kloek, Andrew
Williams, Deryck Jeremy
Salmon, Brandy Leigh
Bradley, John D.

<120> NEMATODE PGM-LIKE SEQUENCES

<130> 12557-003001

<140> US 10/082,894

<141> 2002-02-26

<150> US 60/271,781

<151> 2001-02-27

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<212> DNA

<213> Meloidogyne incognita PGM

<220>

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Val Cys Leu Val Val Ile Asp Gly Trp Gly Leu Ser Asp Glu Gln His	
15 20 25	
ggg aat gca att gct aaa gct aaa acg cct att atg gac aaa ctt tgt	147
Gly Asn Ala Ile Ala Lys Ala Lys Thr Pro Ile Met Asp Lys Leu Cys	
30 35 40	
tct gga aat tgg caa aaa ttg gaa gca cac ggt ctt cat gtt gga ttg	195
Ser Gly Asn Trp Gln Lys Leu Glu Ala His Gly Leu His Val Gly Leu	
45 50 55	
cca gaa ggc tta atg gga aat tct gaa gtt gga cat ttg aat ata gga	243
Pro Glu Gly Leu Met Gly Asn Ser Glu Val Gly His Leu Asn Ile Gly	
60 65 70	
gct gga aga gtt att tat caa gat att gtt cga att aat ttg gct gtt	291
Ala Gly Arg Val Ile Tyr Gln Asp Ile Val Arg Ile Asn Leu Ala Val	
75 80 85 90	

caa cga aac gag ttt gtt aca aat cct cag att gtt gca tca gct gag	339
Gln Arg Asn Glu Phe Val Thr Asn Pro Gln Ile Val Ala Ser Ala Glu	
95 100 105	
cgt gca aag aag ggg agt ggt cga ttg cat tta tta gga ctg gtt agc	387
Arg Ala Lys Lys Gly Ser Gly Arg Leu His Leu Leu Gly Leu Val Ser	
110 115 120	
gat ggt ggt gtc cac tct cat att gat cat ctt ttt gcg ttg ata cgt	435
Asp Gly Gly Val His Ser His Ile Asp His Leu Phe Ala Leu Ile Arg	
125 130 135	
gca ttt aaa caa tta caa gtg cca aag gtt ttc att cac ttt ttt gct	483
Ala Phe Lys Gln Leu Gln Val Pro Lys Val Phe Ile His Phe Phe Ala	
140 145 150	
gat ggt cga gat act tcg cca aca agt gga gct ggt tat ctt gaa caa	531
Asp Gly Arg Asp Thr Ser Pro Thr Ser Gly Ala Gly Tyr Leu Glu Gln	
155 160 165 170	
ctt ctt caa ttt att gct tcg gaa aag tac gga gaa ttg gct act att	579
Leu Leu Gln Phe Ile Ala Ser Glu Lys Tyr Gly Glu Leu Ala Thr Ile	
175 180 185	
act gga cgt tat tat gca atg gat agg gac aaa aga tgg gag cgt att	627
Thr Gly Arg Tyr Tyr Ala Met Asp Arg Asp Lys Arg Trp Glu Arg Ile	
190 195 200	
aag atg gct tat gag gca att gtt gga ggt att gga caa aaa gcc acc	675
Lys Met Ala Tyr Glu Ala Ile Val Gly Gly Ile Gly Gln Lys Ala Thr	
205 210 215	
gtt gat aag gct gtc gat gtt gtt aga gag cga tat gct caa tct gag	723
Val Asp Lys Ala Val Asp Val Val Arg Glu Arg Tyr Ala Gln Ser Glu	
220 225 230	
act gac gaa ttt ctg aaa cca att gtt ttt tcg gac gat ggg cga gta	771
Thr Asp Glu Phe Leu Lys Pro Ile Val Phe Ser Asp Asp Gly Arg Val	
235 240 245 250	
aaa gat gac gat act ctt att ttc ttc aat tat cgt gct gat cgt atg	819
Lys Asp Asp Asp Thr Leu Ile Phe Phe Asn Tyr Arg Ala Asp Arg Met	
255 260 265	
cgt caa att tgt gaa tgt ttg ggt ctc gaa cgt tat aaa gat ctt aat	867
Arg Gln Ile Cys Glu Cys Leu Gly Leu Glu Arg Tyr Lys Asp Leu Asn	
270 275 280	
agt tcg gtt cct cac cct aaa aat att cag att agt ggg atg acc caa	915
Ser Ser Val Pro His Pro Lys Asn Ile Gln Ile Ser Gly Met Thr Gln	
285 290 295	
tac aat aaa gag ttt cca ttt cca tcg tta ttc cca cct gtg act cat	963
Tyr Asn Lys Glu Phe Pro Phe Pro Ser Leu Phe Pro Pro Val Thr His	
300 305 310	

act aat gtg ctt gct gaa tgg ctt gct tct caa gga gtt act caa ttt	1011
Thr Asn Val Leu Ala Glu Trp Leu Ala Ser Gln Gly Val Thr Gln Phe	
315 320 325 330	
cac tgt gcg gaa act gag aag tat cct cat gtt acc ttc ttc ttt aat	1059
His Cys Ala Glu Thr Glu Lys Tyr Pro His Val Thr Phe Phe Phe Asn	
335 340 345	
ggt ggt cga gaa gtt caa ttc caa gat gaa gag cgt tgt atg gtt ccg	1107
Gly Gly Arg Glu Val Gln Phe Gln Asp Glu Glu Arg Cys Met Val Pro	
350 355 360	
tca cca aaa gaa gtt gct aca tat gat tta aaa cca gaa atg aat gct	1155
Ser Pro Lys Glu Val Ala Thr Tyr Asp Leu Lys Pro Glu Met Asn Ala	
365 370 375	
gct gga gtt gcc gaa aaa atg gtc gag caa att gag tca ggc agg cat	1203
Ala Gly Val Ala Glu Lys Met Val Glu Gln Ile Glu Ser Gly Arg His	
380 385 390	
cct ttg gtt atg tgc aat ttt gcg cct cct gac atg gtt gga cat act	1251
Pro Leu Val Met Cys Asn Phe Ala Pro Pro Asp Met Val Gly His Thr	
395 400 405 410	
ggt aaa ttt gaa cct gcc gtc aaa gca tgt caa gct act gac gag gca	1299
Gly Lys Phe Glu Pro Ala Val Lys Ala Cys Gln Ala Thr Asp Glu Ala	
415 420 425	
att gga aag ata ttt gaa gca tgc caa act tat aat tac gtt ctt atg	1347
Ile Gly Lys Ile Phe Glu Ala Cys Gln Thr Tyr Asn Tyr Val Leu Met	
430 435 440	
gtt act tcc gat cat gga aat gct gag aag atg att gct ccc gat ggt	1395
Val Thr Ser Asp His Gly Asn Ala Glu Lys Met Ile Ala Pro Asp Gly	
445 450 455	
agt gaa cat act gca cat acc tgc aat ttg gtc cca ttt act tgc tct	1443
Ser Glu His Thr Ala His Thr Cys Asn Leu Val Pro Phe Thr Cys Ser	
460 465 470	
tcc aaa aca ttt gtt ttt aaa tcg act cca cct act gga gat gat ggc	1491
Ser Lys Thr Phe Val Phe Lys Ser Thr Pro Pro Thr Gly Asp Asp Gly	
475 480 485 490	
aaa gaa cgt gca cga gcc tta cgt gat gtt gca ccg act gtt cta caa	1539
Lys Glu Arg Ala Arg Ala Leu Arg Asp Val Ala Pro Thr Val Leu Gln	
495 500 505	
tta atg ggc tta cct gta ccg ccg gag atg gat ggc gtt cct tta ctt	1587
Leu Met Gly Leu Pro Val Pro Pro Glu Met Asp Gly Val Pro Leu Leu	
510 515 520	
gaa cag aga gga taagaagtta attgacaata ggaaataaat atgagctgct	1639
Glu Gln Arg Gly	
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attacaagca attttaaaaa ttttagtaaa acgagtaatt tttgatatat acatatttag 1699
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<211> 526

<212> PRT

<213> Meloidogyne incognita PGM

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Ala	Lys	Thr	Pro	Ile	Met	Asp	Lys	Leu	Cys	Ser	Gly	Asn	Trp	Gln	Lys
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Leu	Glu	Ala	His	Gly	Leu	His	Val	Gly	Leu	Pro	Glu	Gly	Leu	Met	Gly
	50					55					60				
Asn	Ser	Glu	Val	Gly	His	Leu	Asn	Ile	Gly	Ala	Gly	Arg	Val	Ile	Tyr
	65				70					75				80	
Gln	Asp	Ile	Val	Arg	Ile	Asn	Leu	Ala	Val	Gln	Arg	Asn	Glu	Phe	Val
				85					90					95	
Thr	Asn	Pro	Gln	Ile	Val	Ala	Ser	Ala	Glu	Arg	Ala	Lys	Lys	Gly	Ser
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Gly	Arg	Leu	His	Leu	Leu	Gly	Leu	Val	Ser	Asp	Gly	Gly	Val	His	Ser
	115					120					125				
His	Ile	Asp	His	Leu	Phe	Ala	Leu	Ile	Arg	Ala	Phe	Lys	Gln	Leu	Gln
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Val	Pro	Lys	Val	Phe	Ile	His	Phe	Phe	Ala	Asp	Gly	Arg	Asp	Thr	Ser
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Pro	Thr	Ser	Gly	Ala	Gly	Tyr	Leu	Glu	Gln	Leu	Leu	Gln	Phe	Ile	Ala
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Ser	Glu	Lys	Tyr	Gly	Glu	Leu	Ala	Thr	Ile	Thr	Gly	Arg	Tyr	Tyr	Ala
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Met	Asp	Arg	Asp	Lys	Arg	Trp	Glu	Arg	Ile	Lys	Met	Ala	Tyr	Glu	Ala
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Ile	Val	Gly	Gly	Ile	Gly	Gln	Lys	Ala	Thr	Val	Asp	Lys	Ala	Val	Asp
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Val	Val	Arg	Glu	Arg	Tyr	Ala	Gln	Ser	Glu	Thr	Asp	Glu	Phe	Leu	Lys
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Pro	Ile	Val	Phe	Ser	Asp	Asp	Gly	Arg	Val	Lys	Asp	Asp	Asp	Thr	Leu
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Ile	Phe	Phe	Asn	Tyr	Arg	Ala	Asp	Arg	Met	Arg	Gln	Ile	Cys	Glu	Cys
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Leu	Gly	Leu	Glu	Arg	Tyr	Lys	Asp	Leu	Asn	Ser	Ser	Val	Pro	His	Pro
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Lys	Asn	Ile	Gln	Ile	Ser	Gly	Met	Thr	Gln	Tyr	Asn	Lys	Glu	Phe	Pro
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Phe	Pro	Ser	Leu	Phe	Pro	Pro	Val	Thr	His	Thr	Asn	Val	Leu	Ala	Glu
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Trp	Leu	Ala	Ser	Gln	Gly	Val	Thr	Gln	Phe	His	Cys	Ala	Glu	Thr	Glu
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Lys	Tyr	Pro	His	Val	Thr	Phe	Phe	Phe	Asn	Gly	Gly	Arg	Glu	Val	Gln
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Phe	Gln	Asp	Glu	Glu	Arg	Cys	Met	Val	Pro	Ser	Pro	Lys	Glu	Val	Ala
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Thr	Tyr	Asp	Leu	Lys	Pro	Glu	Met	Asn	Ala	Ala	Gly	Val	Ala	Glu	Lys
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Met Val Glu Gln Ile Glu Ser Gly Arg His Pro Leu Val Met Cys Asn
 385 390 395 400
 Phe Ala Pro Pro Asp Met Val Gly His Thr Gly Lys Phe Glu Pro Ala
 405 410 415
 Val Lys Ala Cys Gln Ala Thr Asp Glu Ala Ile Gly Lys Ile Phe Glu
 420 425 430
 Ala Cys Gln Thr Tyr Asn Tyr Val Leu Met Val Thr Ser Asp His Gly
 435 440 445
 Asn Ala Glu Lys Met Ile Ala Pro Asp Gly Ser Glu His Thr Ala His
 450 455 460
 Thr Cys Asn Leu Val Pro Phe Thr Cys Ser Ser Lys Thr Phe Val Phe
 465 470 475 480
 Lys Ser Thr Pro Pro Thr Gly Asp Asp Gly Lys Glu Arg Ala Arg Ala
 485 490 495
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<211> 539

<212> PRT

<213> Caenorhabditis elegans PGM

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 Leu Ile Val Ile Asp Gly Trp Gly Val Ser Glu Asp Pro Tyr Gly Asn
 35 40 45
 Ala Ile Leu Asn Ala Gln Thr Pro Val Met Asp Lys Leu Cys Ser Gly
 50 55 60
 Asn Trp Ala Gln Ile Glu Ala His Gly Leu His Val Gly Leu Pro Glu
 65 70 75 80
 Gly Leu Met Gly Asn Ser Glu Val Gly His Leu Asn Ile Gly Ala Gly
 85 90 95
 Arg Val Ile Tyr Gln Asp Ile Val Arg Ile Asn Leu Ala Val Lys Asn
 100 105 110
 Asn Lys Phe Val Thr Asn Glu Ser Leu Val Asp Ala Cys Asp Arg Ala
 115 120 125
 Lys Asn Gly Asn Gly Arg Leu His Leu Ala Gly Leu Val Ser Asp Gly
 130 135 140
 Gly Val His Ser His Ile Asp His Met Phe Ala Leu Val Lys Ala Ile
 145 150 155 160
 Lys Glu Leu Gly Val Pro Glu Leu Tyr Leu His Phe Tyr Gly Asp Gly
 165 170 175
 Arg Asp Thr Ser Pro Asn Ser Gly Val Gly Phe Leu Glu Gln Thr Leu
 180 185 190
 Glu Phe Leu Glu Lys Thr Thr Gly Tyr Gly Lys Leu Ala Thr Val Val
 195 200 205
 Gly Arg Tyr Tyr Ala Met Asp Arg Asp Asn Arg Trp Glu Arg Ile Asn
 210 215 220
 Val Ala Tyr Glu Ala Met Ile Gly Gly Val Gly Glu Thr Ser Asp Glu
 225 230 235 240
 Ala Gly Val Val Glu Val Val Arg Lys Arg Tyr Ala Ala Asp Glu Thr
 245 250 255

Asp Glu Phe Leu Lys Pro Ile Ile Leu Gln Gly Glu Lys Gly Arg Val
 260 265 270
 Gln Asn Asp Asp Thr Ile Ile Phe Phe Asp Tyr Arg Ala Asp Arg Met
 275 280 285
 Arg Glu Ile Ser Ala Ala Met Gly Met Asp Arg Tyr Lys Asp Cys Asn
 290 295 300
 Ser Lys Leu Ala His Pro Ser Asn Leu Gln Val Tyr Gly Met Thr Gln
 305 310 315 320
 Tyr Lys Ala Glu Phe Pro Phe Lys Ser Leu Phe Pro Pro Ala Ser Asn
 325 330 335
 Lys Asn Val Leu Ala Glu Trp Leu Ala Glu Gln Lys Val Ser Gln Phe
 340 345 350
 His Cys Ala Glu Thr Glu Lys Tyr Ala His Val Thr Phe Phe Phe Asn
 355 360 365
 Gly Gly Leu Glu Lys Gln Phe Glu Gly Glu Glu Arg Cys Leu Val Pro
 370 375 380
 Ser Pro Lys Val Ala Thr Tyr Asp Leu Gln Pro Glu Met Ser Ala Ala
 385 390 395 400
 Gly Val Ala Asp Lys Met Ile Glu Gln Leu Glu Ala Gly Thr His Pro
 405 410 415
 Phe Ile Met Cys Asn Phe Ala Pro Pro Asp Met Val Gly His Thr Gly
 420 425 430
 Val Tyr Glu Ala Ala Val Lys Ala Cys Glu Ala Thr Asp Ile Ala Ile
 435 440 445
 Gly Arg Ile Tyr Glu Ala Thr Gln Lys His Gly Tyr Ser Leu Met Val
 450 455 460
 Thr Ala Asp His Gly Asn Ala Glu Lys Met Lys Ala Pro Asp Gly Gly
 465 470 475 480
 Lys His Thr Ala His Thr Cys Tyr Arg Val Pro Leu Thr Leu Ser His
 485 490 495
 Pro Gly Phe Lys Phe Val Asp Pro Ala Asp Arg His Pro Ala Leu Cys
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<210> 4

<211> 526

<212> PRT

<213> Meloidogyne icognita PGM

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 20 25 30
 Ala Lys Thr Pro Ile Met Asp Lys Leu Cys Ser Gly Asn Trp Gln Lys
 35 40 45
 Leu Glu Ala His Gly Leu His Val Gly Leu Pro Glu Gly Leu Met Gly
 50 55 60
 Asn Ser Glu Val Gly His Leu Asn Ile Gly Ala Gly Arg Val Ile Tyr
 65 70 75 80
 Gln Asp Ile Val Arg Ile Asn Leu Ala Val Gln Arg Asn Glu Phe Val
 85 90 95
 Thr Asn Pro Gln Ile Val Ala Ser Ala Glu Arg Ala Lys Lys Gly Ser
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Val	Pro	Lys	Val	Phe	Ile	His	Phe	Phe	Ala	Asp	Gly	Arg	Asp	Thr	Ser
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Pro	Thr	Ser	Gly	Ala	Gly	Tyr	Leu	Glu	Gln	Leu	Leu	Gln	Phe	Ile	Ala
				165					170					175	
Ser	Glu	Lys	Tyr	Gly	Glu	Leu	Ala	Thr	Ile	Thr	Gly	Arg	Tyr	Tyr	Ala
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Val	Val	Arg	Glu	Arg	Tyr	Ala	Gln	Ser	Glu	Thr	Asp	Glu	Phe	Leu	Lys
					230					235					240
Pro	Ile	Val	Phe	Ser	Asp	Asp	Gly	Arg	Val	Lys	Asp	Asp	Asp	Thr	Leu
				245					250					255	
Ile	Phe	Phe	Asn	Tyr	Arg	Ala	Asp	Arg	Met	Arg	Gln	Ile	Cys	Glu	Cys
			260				265						270		
Leu	Gly	Leu	Glu	Arg	Tyr	Lys	Asp	Leu	Asn	Ser	Ser	Val	Pro	His	Pro
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Lys	Asn	Ile	Gln	Ile	Ser	Gly	Met	Thr	Gln	Tyr	Asn	Lys	Glu	Phe	Pro
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Phe	Pro	Ser	Leu	Phe	Pro	Pro	Val	Thr	His	Thr	Asn	Val	Leu	Ala	Glu
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Trp	Leu	Ala	Ser	Gln	Gly	Val	Thr	Gln	Phe	His	Cys	Ala	Glu	Thr	Glu
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Lys	Tyr	Pro	His	Val	Thr	Phe	Phe	Phe	Asn	Gly	Gly	Arg	Glu	Val	Gln
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Phe	Gln	Asp	Glu	Glu	Arg	Cys	Met	Val	Pro	Ser	Pro	Lys	Glu	Val	Ala
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Met	Val	Glu	Gln	Ile	Glu	Ser	Gly	Arg	His	Pro	Leu	Val	Met	Cys	Asn
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Phe	Ala	Pro	Pro	Asp	Met	Val	Gly	His	Thr	Gly	Lys	Phe	Glu	Pro	Ala
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Val	Lys	Ala	Cys	Gln	Ala	Thr	Asp	Glu	Ala	Ile	Gly	Lys	Ile	Phe	Glu
			420					425					430		
Ala	Cys	Gln	Thr	Tyr	Asn	Tyr	Val	Leu	Met	Val	Thr	Ser	Asp	His	Gly
		435					440					445			
Asn	Ala	Glu	Lys	Met	Ile	Ala	Pro	Asp	Gly	Ser	Glu	His	Thr	Ala	His
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Thr	Cys	Asn	Leu	Val	Pro	Phe	Thr	Cys	Ser	Ser	Lys	Thr	Phe	Val	Phe
				470						475					480
Lys	Ser	Thr	Pro	Pro	Thr	Gly	Asp	Asp	Gly	Lys	Glu	Arg	Ala	Arg	Ala
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Leu	Arg	Asp	Val	Ala	Pro	Thr	Val	Leu	Gln	Leu	Met	Gly	Leu	Pro	Val
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Pro	Pro	Glu	Met	Asp	Gly	Val	Pro	Leu	Leu	Glu	Gln	Arg	Gly		
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<213> Artificial Sequence

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<223> Vector polylinker primer

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22

<210> 6

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Vector polylinker primer

<400> 6

aattaaccct cactaaaggg

20

<210> 7

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Universal primer to poly A tail

<400> 7

gagagagaga gagagagaga actagtctcg agtttttttt tttttttttt

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<210> 8

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Nematode transpliced leader

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<210> 9

<211> 18

<212> DNA

<213> Artificial Sequence

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<223> Mi PGM (codon 234-239)

<400> 9

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18

<210> 10

<211> 18

<212> DNA

<213> Artificial Sequence

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 <223> Mi PGM (codon 234-239)

<400> 10
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<210> 11
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 <212> DNA
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<220>
 <223> Mi PGM (codon 15-20)

<400> 11
 gttattgatg gatgggg 17

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 <212> DNA
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 <223> Mi PGM (codon 15-20)

<400> 12
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<210> 13
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 <223> Mi PGM (codon 59-65)

<400> 13
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<210> 14
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 <223> Mi PGM (codon 59-65)

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